What is claimed is:

1. Isolated polynucleotide containing a polynucleotide sequence coding for the sucC- and/or sucD-gene, selected from the group comprising

a) Polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,

b) Polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 3,

c) Polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to that of the amino acid sequence of SEQ ID No. 2,

d) Polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to that of the amino acid sequence of SEQ ID No. 3,

e) Polynucleotide that is complementary to the polynucleotides of a), b), c) or d), and

f) Polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequences of a), b), c), d) or e),

the polypeptide preferably having the activity of succinyl-CoA synthetase.

2. Polynucleotides according to claim 1, wherein the polynucleotide is a preferably recombinant DNA that is replicable in coryneform bacteria.

3. Polynucleotides according to claim 1, wherein the polynucleotide is a RNA.

4. Polynucleotides according to claim 2, containing the nucleic acid sequence as shown in SEQ ID NO 1.

5. Replicable DNA according to claim 2, containing

(i) the nucleotide sequence shown in SEQ ID NO 1, or

(ii) at least one sequence that corresponds to the sequences (i) within the region of degeneration of the genetic code, or

(iii) at least one sequence that hybridizes with the sequences that are complementary to the sequences (i) or (ii) , and optionally

(iv) functionally neutral sense mutations in (i).

6. Replicable DNA according to claim 5, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.

7. Polynucleotide sequence according to claim 1 that codes for a polypeptide that contains the amino acid sequence shown in SEQ ID No. 2.

8. Coryneform bacteria in which the sucC- and/or sucD-gene is/are attenuated.

9. Process for producing L-amino acids, in particular L-lysine and/or L-glutamate, wherein the following steps are carried out:

a) fermentation of the bacteria producing the desired L-amino acid, in which first of all the sucC- and/or sucD-gene or nucleotide sequences coding therefor are attenuated, in particular switched off;

b) enrichment of the L-amino acid in the medium or in the bacterial cells, and

c) isolation of the L-amino acid.

10. Process according to claim 9, wherein bacteria are used in which in addition further genes of the biosynthesis pathway of the desired L-amino acid are enhanced.

11. Process according to claim 9, wherein bacteria are used in which the metabolic pathways that reduce the formation of the desired L-amino acid are at least partially switched off.

12. Process according to claim 9, wherein the expression of the polynucleotide(s) that codes for the sucC- and/or sucD-genes is attenuated, in particular is switched off.

13. Process according to claim 9, wherein the catalytic properties of the polypeptide (enzyme protein) for which the polynucleotides sucC and sucD code are reduced.

14. Process according to claim 9, wherein for the production of L-amino acids microorganisms are fermented in which at the same time one or more of the genes selected from the following group is/are enhanced and/or overexpressed:

14.1 the dapA-gene coding for dihydrodipicolinate synthase,

14.2 the pyc-gene coding for pyruvate carboxylase,

14.3 the gap-gene coding for glyceraldehyde-3-phosphate dehydrogenase,

14.4 the gene tpi coding for triose phosphate isomerase,

14.5 the gene pgk coding for 3-phosphoglycerate kinase,

14.6 the mqo-gene coding for malate:quinone oxidoreductase,

14.7 the lysE-gene coding for L-lysine export,

14.8 the gene lysC coding for a feedback resistant aspartate kinase,

14.9 the gene zwa1 coding for the Zwa1-protein.

15. Process according to claim 9, wherein for the production of L-amino acids coryneform microorganisms are fermented, in which at the same time one or more of the genes selected from the following group is/are attenuated:

15.1 the gene pck coding for phosphoenol pyruvate carboxykinase,

15.2 the gene pgi coding for glucose-6-phosphate isomerase,

15.3 the gene poxB coding for pyruvate-oxidase,

15.4 the gene zwa2 coding for the Zwa2-Protein.

16. Coryneform bacteria containing a vector that carries parts of the polynucleotide according to claim 1, but at least 15 successive nucleotides of the claimed sequence.

17. DNA derived from coryneform bacteria that code for SucC proteins, whose amino acid sequence (SEQ ID No. 2) contains one or more replacements selected from the group: replacement at position 22 by any other proteinogenic amino acid except L-proline, replacement at position 44 by any other proteinogenic amino acid except glycine, and replacement at position 170 by any other proteinogenic amino acid except L-alanine.

18. DNA according to claim 17, wherein this codes for SucC proteins whose amino acid sequences contain one or more replacements selected from the group: L-proline at position 22 by L-serine, glycine at position 44 by L-glutamic acid, and L-alanine at position 170 by L-threonine.

19. DNA according to claim 18, wherein this codes for a SucC protein whose amino acid sequence contains L-serine at position 22, L-glutamic acid at position 44, and L-threonine at position 170, as illustrated in SEQ ID No.5.

20. DNA according to claim 17, wherein this contains the nucleobase thymine at position 64, the nucleobase adenine at position 131, and the nucleobase adenine at position 508, as illustrated in SEQ ID No 4.

21. Coryneforme bacteria that contain a DNA according to claim 17, 18, 19 or 20.

22. Integration vector pCRBluntsucCint, that

22.1 carries a 0.55 kb long internal fragment of the sucC-gene,

22.2 whose restriction map is reproduced in Fig. 1, and

22.3 that in the E. coli strain TOP10/pCRBluntsucCint has been filed under No. DSM 13750 at the German Collection for Microorganisms and Cell Cultures.

23. Plasmid vector pK18mobsacBsucDdel that

23.1 carries a sucD-gene containing a deletion,

23.2 whose restriction map is reproduced in Fig. 2, and

23.3 that in the E. coli strain DH5αmcr/ pK18mobsacBsucDdel has been filed under No. DSM 13749 at the German Collection for Microorganisms and Cell Cultures.

24. Process according to one or more of the preceding claims, wherein microorganisms of the type Corynebacterium glutamicum are used.

25. Process for detecting RNA, cDNA and DNA in order to isolate nucleic acids and/or polynucleotides or genes that code for succinyl-CoA synthase or that have a high degree of similarity to the sequence of the sucC- and/or sucD-gene, wherein the polynucleotide containing the polynucleotide sequences according to claims 1, 2, 3 or 4, is used as hybridization probe.